TEAM 7

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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/538,709*

DATE: 12/01/95
TIME: 17:15:21

INPUT SET: S7645.raw

> **This Raw Listing contains the General Information Section and up to the first 5 pages.**

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 1                                    SEQUENCE LISTING            ENTERED
 2
 3    (1)     General Information:
 4
 5        (i) APPLICANT: Cerretti, Douglas P.
 6
 7       (ii) TITLE OF INVENTION: Cytokine Designated as LERK-6
 8
 9      (iii) NUMBER OF SEQUENCES: 8
10
11       (iv) CORRESPONDENCE ADDRESS:
12            (A)  ADDRESSEE: Immunex Corporation
13            (B)  STREET: 51 University Street
14            (C)  CITY: Seattle
15            (D)  STATE: WA
16            (E)  COUNTRY: USA
17            (F)  ZIP: 98101
18
19        (v) COMPUTER READABLE FORM:
20            (A)  MEDIUM TYPE: Floppy disk
21            (B)  COMPUTER: Apple Macintosh
22            (C)  OPERATING SYSTEM: System 7.1
23            (D)  SOFTWARE: PatentIn Release #1.0, Version #1.25
24
25       (vi) CURRENT APPLICATION DATA:
26            (A)  APPLICATION NUMBER: US --to be assigned--
27            (B)  FILING DATE:
28            (C)  CLASSIFICATION:
29
30     (viii) ATTORNEY/AGENT INFORMATION:
31            (A)  NAME: Malaska, Stephen L.
32            (B)  REGISTRATION NUMBER: 32,655
33            (C)  REFERENCE/DOCKET NUMBER: 2826
34
35       (ix) TELECOMMUNICATION INFORMATION:
36            (A)  TELEPHONE: (206) 587-0430
37            (B)  TELEFAX: (206) 233-0644
38
39
40    (2) INFORMATION FOR SEQ ID NO:1:
41
42        (i) SEQUENCE CHARACTERISTICS:
43            (A)  LENGTH: 555 base pairs
44            (B)  TYPE: nucleic acid
45            (C)  STRANDEDNESS: single
46            (D)  TOPOLOGY: linear
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47
48        (ii) MOLECULE TYPE: cDNA
49
50       (iii) HYPOTHETICAL: NO
51
52        (iv) ANTI-SENSE: NO
53
54
55       (vii) IMMEDIATE SOURCE:
56               (B) CLONE: LERK-6
57
58        (ix) FEATURE:
59               (A) NAME/KEY: CDS
60               (B) LOCATION: 1..552
61
62
63        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65    GCC CGG GCC AAC GCT GAC CGA TAC GCA GTC TAC TGG AAC CGT AGC AAC        48
66    Ala Arg Ala Asn Ala Asp Arg Tyr Ala Val Tyr Trp Asn Arg Ser Asn
67     1               5                  10                  15
68
69    CCC AGG TTT CAG GTG AGC GCT GTG GGT GAT GGC GGC GGC TAT ACC GTG        96
70    Pro Arg Phe Gln Val Ser Ala Val Gly Asp Gly Gly Gly Tyr Thr Val
71                20                  25                  30
72
73    GAG GTG AGC ATC AAC GAC TAC CTG GAT ATC TAC TGC CCA CAC TAC GGG       144
74    Glu Val Ser Ile Asn Asp Tyr Leu Asp Ile Tyr Cys Pro His Tyr Gly
75             35                  40                  45
76
77    GCG CCG CTG CCC CCG GCT GAG CGC ATG GAG CGG TAC ATC CTG TAC ATG       192
78    Ala Pro Leu Pro Pro Ala Glu Arg Met Glu Arg Tyr Ile Leu Tyr Met
79          50                  55                  60
80
81    GTG AAT GGT GAG GGC CAC GCC TCC TGT GAC CAC CGG CAG CGA GGC TTC       240
82    Val Asn Gly Glu Gly His Ala Ser Cys Asp His Arg Gln Arg Gly Phe
83     65                  70                  75                  80
84
85    AAG CGC TGG GAA TGC AAC CGG CCC GCA GCG CCC GGG GGA CCC CTC AAG       288
86    Lys Arg Trp Glu Cys Asn Arg Pro Ala Ala Pro Gly Gly Pro Leu Lys
87                  85                  90                  95
88
89    TTC TCA GAG AAG TTC CAA CTC TTC ACC CCC TTT TCC CTG GGC TTT GAG       336
90    Phe Ser Glu Lys Phe Gln Leu Phe Thr Pro Phe Ser Leu Gly Phe Glu
91                100                 105                 110
92
93    TTC CGG CCT GGC CAC GAA TAC TAC TAC ATC TCT GCC ACA CCT CCC AAC       384
94    Phe Arg Pro Gly His Glu Tyr Tyr Tyr Ile Ser Ala Thr Pro Pro Asn
95                115                 120                 125
96
97    CTC GTG GAC CGA CCC TGC CTG CGA CTC AAG GTT TAT GTG CGT CCA ACC       432
98    Leu Val Asp Arg Pro Cys Leu Arg Leu Lys Val Tyr Val Arg Pro Thr
99                130                 135                 140
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100
101     AAT GAG ACC CTG TAT GAG GCT CCA GAG CCC ATC TTC ACC AGT AAC AGC        480
102     Asn Glu Thr Leu Tyr Glu Ala Pro Glu Pro Ile Phe Thr Ser Asn Ser
103     145                 150                 155                 160
104
105     TCC TGC AGC GGC CTG GGT GGC TGC CAC CTC TTC CTC ACC ACC GTC CCT        528
106     Ser Cys Ser Gly Leu Gly Gly Cys His Leu Phe Leu Thr Thr Val Pro
107                     165                 170                 175
108
109     GTG CTG TGG TCC CTT CTG GGC TCC TAG                                    555
110     Val Leu Trp Ser Leu Leu Gly Ser
111                     180
112
113
114     (2) INFORMATION FOR SEQ ID NO:2:
115
116             (i) SEQUENCE CHARACTERISTICS:
117                     (A) LENGTH: 184 amino acids
118                     (B) TYPE: amino acid
119                     (D) TOPOLOGY: linear
120
121             (ii) MOLECULE TYPE: protein
122
123             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
124
125     Ala Arg Ala Asn Ala Asp Arg Tyr Ala Val Tyr Trp Asn Arg Ser Asn
126       1                 5                 10                15
127
128     Pro Arg Phe Gln Val Ser Ala Val Gly Asp Gly Gly Gly Tyr Thr Val
129                     20                 25                 30
130
131     Glu Val Ser Ile Asn Asp Tyr Leu Asp Ile Tyr Cys Pro His Tyr Gly
132                 35                 40                 45
133
134     Ala Pro Leu Pro Pro Ala Glu Arg Met Glu Arg Tyr Ile Leu Tyr Met
135             50                 55                 60
136
137     Val Asn Gly Glu Gly His Ala Ser Cys Asp His Arg Gln Arg Gly Phe
138       65                 70                 75                80
139
140     Lys Arg Trp Glu Cys Asn Arg Pro Ala Ala Pro Gly Gly Pro Leu Lys
141                     85                 90                 95
142
143     Phe Ser Glu Lys Phe Gln Leu Phe Thr Pro Phe Ser Leu Gly Phe Glu
144                     100                105                110
145
146     Phe Arg Pro Gly His Glu Tyr Tyr Tyr Ile Ser Ala Thr Pro Pro Asn
147                 115                 120                125
148
149     Leu Val Asp Arg Pro Cys Leu Arg Leu Lys Val Tyr Val Arg Pro Thr
150             130                 135                 140
151
152     Asn Glu Thr Leu Tyr Glu Ala Pro Glu Pro Ile Phe Thr Ser Asn Ser
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INPUT SET: S7645.raw

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153    145                150                155                160
154
155    Ser Cys Ser Gly Leu Gly Gly Cys His Leu Phe Leu Thr Thr Val Pro
156                    165                170                175
157
158    Val Leu Trp Ser Leu Leu Gly Ser
159                180
160
161    (2) INFORMATION FOR SEQ ID NO:3:
162
163         (i) SEQUENCE CHARACTERISTICS:
164              (A) LENGTH: 28 base pairs
165              (B) TYPE: nucleic acid
166              (C) STRANDEDNESS: single
167              (D) TOPOLOGY: linear
168
169        (ii) MOLECULE TYPE: cDNA
170
171
172
173        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
174
175    GATATTTACT GCCCGCACTA CAACAGCT                                    28
176
177    (2) INFORMATION FOR SEQ ID NO:4:
178
179         (i) SEQUENCE CHARACTERISTICS:
180              (A) LENGTH: 25 base pairs
181              (B) TYPE: nucleic acid
182              (C) STRANDEDNESS: single
183              (D) TOPOLOGY: linear
184
185        (ii) MOLECULE TYPE: cDNA
186
187       (iii) HYPOTHETICAL: NO
188
189        (iv) ANTI-SENSE: NO
190
191
192
193        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
194
195    AGAGAAGGCG CTGTAGCGCT GGAAC                                       25
196
197    (2) INFORMATION FOR SEQ ID NO:5:
198
199         (i) SEQUENCE CHARACTERISTICS:
200              (A) LENGTH: 31 base pairs
201              (B) TYPE: nucleic acid
202              (C) STRANDEDNESS: single
203              (D) TOPOLOGY: linear
204
205        (ii) MOLECULE TYPE: cDNA
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INPUT SET: S7645.raw

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206
207        (iii) HYPOTHETICAL: NO
208
209         (iv) ANTI-SENSE: NO
210
211
212
213        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
214
215   ACGTAGTCTA CTGGAACTCC AGTAACCCCA G                              31
216
217   (2) INFORMATION FOR SEQ ID NO:6:
218
219        (i) SEQUENCE CHARACTERISTICS:
220            (A) LENGTH: 34 base pairs
221            (B) TYPE: nucleic acid
222            (C) STRANDEDNESS: single
223            (D) TOPOLOGY: linear
224
225        (ii) MOLECULE TYPE: cDNA
226
227       (iii) HYPOTHETICAL: NO
228
229        (iv) ANTI-SENSE: NO
230
231
232
233        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
234
235   AGCCTCAAGC ACTGGCCAGA ACTCTCTCTG GAGT                           34
236
237
238   (2) INFORMATION FOR SEQ ID NO:7:
239
240        (i) SEQUENCE CHARACTERISTICS:
241            (A) LENGTH: 314 base pairs
242            (B) TYPE: nucleic acid
243            (C) STRANDEDNESS: single
244            (D) TOPOLOGY: linear
245
246        (ii) MOLECULE TYPE: cDNA to mRNA
247
248       (iii) HYPOTHETICAL: NO
249
250        (iv) ANTI-SENSE: NO
251
252
253        (ix) FEATURE:
254            (A) NAME/KEY: CDS
255            (B) LOCATION: 2..313
256
257
258        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/538,709*

DATE: 12/01/95
TIME: 17:15:32

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Line	Error	Original Text
26	Wrong application Serial Number	(A) APPLICATION NUMBER: US --to be assigned--